Galaxy @ CRUK-CI

http://galaxy.cruk.cam.ac.uk/

Anne Pajon, Bioinformatics Core

Reproducible Research . User Experiences

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Definition

Reproducibility is the ability that an analysis described in sufficient detail ***can*** be precisely reproduced.
(by another person, in another environment)

Core tasks

1. Capture the precise description of the analysis
2. Assemble all the necessary data and software dependencies needed by the described analysis
3. Combine the above to verify the analysis

Key problems

Missing software, version, parameters (even data)

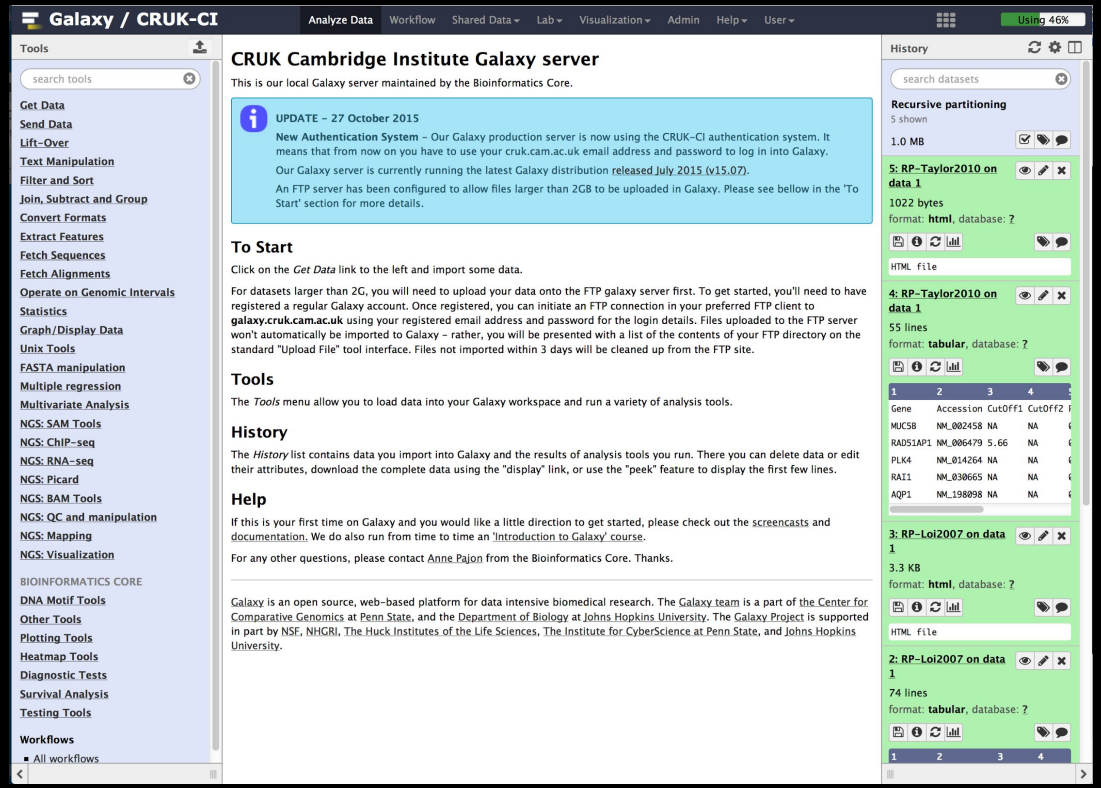
- **Tools**: inaccessible, hard to record details
- **Datasets**: not all available, difficult to access
- **Publication**: results, data, methods separate

50 papers citing BWA randomly selected from 378 published in 2011
Nature Reviews Genetics 13, 667-672 (September 2012) | doi:10.1038/nrg3305

- **31** provide no version and no settings
- **8** list versions, **4** list settings, **7** list versions and settings
- **26** do not provide access to data

Galaxy web-platform for bioinformatics analysis

- Integrate existing tools into a uniform framework
- **Accessible**
  - Users without programming experience can easily run tools
- **Reproducible**
  - History system tracks multisteps analysis
  - Any user can repeat and understand a complete computational analysis



Galaxy tracks every steps of every analysis

- Exact parameters of a step can always be inspected, and easily rerun

RP-Taylor2010 Recursive partitioning on prostate cancer dataset (Galaxy Tool Version 1.0.0) Options

Source file

1: survival_genes.tabular

File containing a list of gene symbols, must be tabular format

Column

Column: 2

Column containing gene symbols

Surgical margin status

Negative

Filter expression data on surgical margin status

Groups

Primary

Filter on group either Primary or Primary + metastatic (all)

Gleason Grade

All

Filter on Gleason grade, 5-6 (low), 7-9 (high) or 5-9 (all)

Pathological T stage

All

Filter on pathological t-stage, T2, T3/T4 or all

Execute

4: RP-Taylor2010 on data 1

55 lines

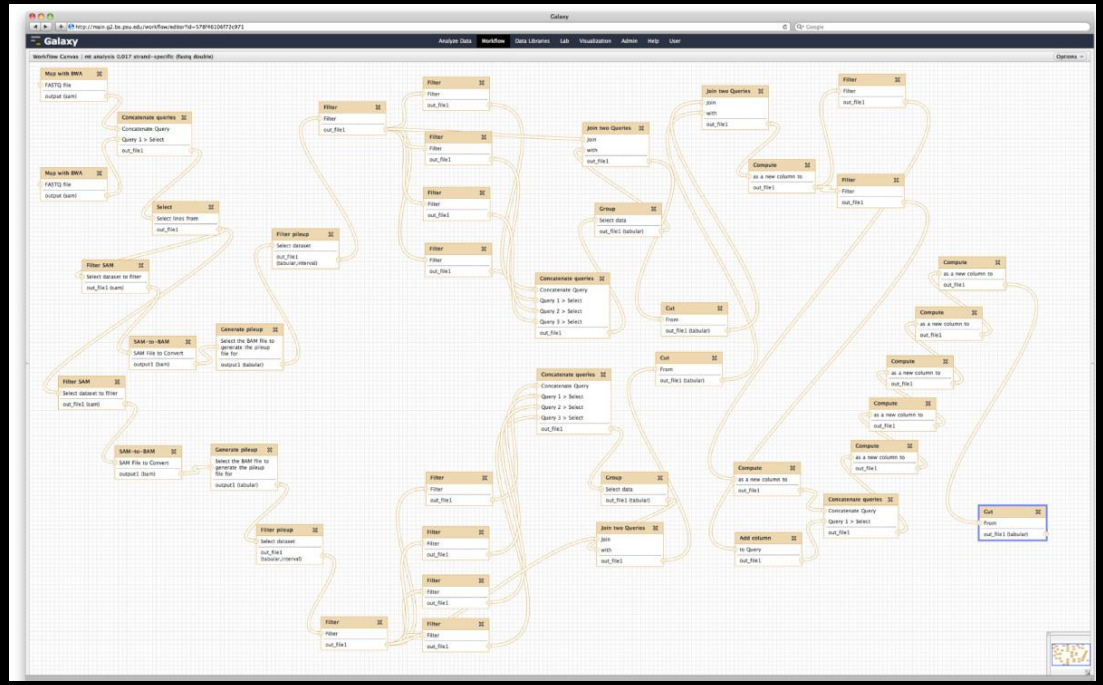
format: **tabular**, database: ?

Run this job again

	3	4
Gene	Accession	CutOff1	CutOff2
MUC5B	NM_002458	NA	NA
RAD51AP1	NM_006479	5.66	NA
PLK4	NM_014264	NA	NA
RAI1	NM_030665	NA	NA
AQP1	NM_198098	NA	NA

Galaxy workflow system

- **Workflows** can be constructed from scratch *or* extracted from existing analysis histories
- Facilitate reuse, as well as providing precise **reproducibility** of a complex analysis



Workflow for finding heteroplasmic sites from Illumina data.
This workflow can be accessed, used, and edited at **http://usegalaxy.org/heteroplasmy**.
Goto et al. Genome Biology 2011 12:R59 | doi:10.1186/gb-2011-12-6-r59

Galaxy data and tool sharing

Repository revision

7 (2015-10-09) *repository tip*

Select a revision to inspect and download versions of Galaxy utilities from this repository.

Repository **tophat2**

Name: tophat2

Owner: devteam

Synopsis: Tophat – fast splice junction mapper for RNA-Seq reads

TopHat is a fast splice junction mapper for RNA-Seq reads. It aligns RNA-Seq reads to mammalian-sized genomes using the ultra high-throughput short read aligner Bowtie(2), and then analyzes the mapping results to identify splice junctions between exons.

Content homepage: http://ccb.jhu.edu/software/tophat/index.shtml

Development repository: https://github.com/galaxyproject/tools-devteam/tree/master/tools/tophat2

Link to this repository: https://toolshed.g2.bx.psu.edu/view/devteam/tophat2/4eb3c3beb9c7

Clone this repository: `hg clone https://toolshed.g2.bx.psu.edu/repos/devteam/tophat2`

Type: unrestricted

Revision: 7:4eb3c3beb9c7

This revision can be installed: True

Times cloned / installed: 2125

Dependencies of this repository

Repository dependencies – *installation of these additional repositories is required*

Repository **package_bowtie_2_2_5** revision **30bd7eaeddbf** owned by **iuc**

Repository **package_tophat_2_0_14** revision **b13271391f95** owned by **iuc**

Tool dependencies – *repository tools require handling of these dependencies*

Name	Version	Type
bowtie2	2.2.5	package
tophat	2.0.14	package

Galaxy items - histories, workflows, visualizations, and pages - can be shared with other people

Galaxy tools - can be published and shared using the tool shed

https://toolshed.g2.bx.psu.edu/

Galaxy is an open-source, web-based, data integration and analysis platform for life science research.

Galaxy enables bench scientists to create, share, and publish sophisticated, **reproducible** bioinformatic analyses without requiring researchers to learn command line interfaces, or Unix system management skills.

Galaxy can be accessed through the project's public server, or on one of the over 60 publicly accessible Galaxy servers. Galaxy can also be installed locally, and on cloud infrastructures.

https://usegalaxy.org/

http://galaxy.cruk.cam.ac.uk/

http://galaxycam.github.io/